

1635

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TECH CENTER 1600/2900



#10/Raw  
Say  
listing

1600

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/840,704A

DATE: 11/21/2002  
TIME: 11:22:39

Input Set : F:\SEQLIST.txt  
Output Set: N:\CRF4\11212002\I840704A.raw

4 <110> APPLICANT: Dedhar, Shoukat  
 5 Hannigan, Greg  
 7 <120> TITLE OF INVENTION: Integrin-Linked Kinase and its Uses  
 10 <130> FILE REFERENCE: KINE-001CON2  
 12 <140> CURRENT APPLICATION NUMBER: US 09/840,704A  
 13 <141> CURRENT FILING DATE: 2001-04-23  
 15 <150> PRIOR APPLICATION NUMBER: 60/009,074  
 16 <151> PRIOR FILING DATE: 1995-12-21  
 18 <150> PRIOR APPLICATION NUMBER: 08/752,345  
 19 <151> PRIOR FILING DATE: 1996-11-19  
 21 <150> PRIOR APPLICATION NUMBER: 08/955,841  
 22 <151> PRIOR FILING DATE: 1997-10-21  
 24 <150> PRIOR APPLICATION NUMBER: 09/390,425  
 25 <151> PRIOR FILING DATE: 1999-09-03  
 27 <150> PRIOR APPLICATION NUMBER: 09/566,906  
 28 <151> PRIOR FILING DATE: 2000-05-09  
 30 <160> NUMBER OF SEQ ID NOS: 21  
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 34 <210> SEQ ID NO: 1  
 35 <211> LENGTH: 1789  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Homo sapiens  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: CDS  
 41 <222> LOCATION: (157)...(1512)  
 W--> 43 <221> NAME/KEY: Other  
 44 <222> LOCATION: (0)...(0)  
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 47 gaatttcatct gtcgactgct accacgggag ttcccccggag aaggatcctg cagcccgagt 60  
 48 cccgaggata aagctgggg ttcatccccc ttccctggat cactccacag tcctcaggct 120  
 49 tcccccaatcc agggactcg ggcggccggac gctgt atg gac gac att ttc act 174  
 50 Met Asp Asp Ile Phe Thr  
 51 1 5  
 53 cag tgc cgg gag ggc aac gca gtc gcc gtt cgc ctg tgg ctg gac aac 222  
 54 Gln Cys Arg Glu Gly Asn Ala Val Ala Val Arg Leu Trp Leu Asp Asn  
 55 10 15 20  
 57 acg gag aac gac ctc aac cag ggg gac gat cat ggc ttc tcc ccc ttg 270  
 58 Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp His Gly Phe Ser Pro Leu  
 59 25 30 35  
 61 cac tgg gcc tgc cga gag ggc cgc tct gct gtg gtt gag atg ttg atc  
 62 His Trp Ala Cys Arg Glu Gly Arg Ser Ala Val Val Glu Met Leu Ile  
 63 40 45 50  
 65 atg cgg ggg gca cgg atc aat gta atg aac cgt ggg gat gac acc ccc 318  
 366

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66	Met	Arg	Gly	Ala	Arg	Ile	Asn	Val	Met	Asn	Arg	Gly	Asp	Asp	Thr	Pro	
67	55					60			65						70		
69	ctg	cat	ctg	gca	gcc	agt	cat	gga	cac	cgt	gat	att	gta	cag	aag	cta	414
70	Leu	His	Leu	Ala	Ala	Ser	His	Gly	His	Arg	Asp	Ile	Val	Gln	Lys	Leu	
71				75					80						85		
73	ttg	cag	tac	aag	gca	gac	atc	aat	gca	gtg	aat	gaa	cac	ggg	aat	gtg	462
74	Leu	Gln	Tyr	Lys	Ala	Asp	Ile	Asn	Ala	Val	Asn	Glu	His	Gly	Asn	Val	
75				90					95						100		
77	ccc	ctg	cac	tat	gcc	tgt	ttt	tgg	ggc	caa	gat	caa	gtg	gca	gag	gac	510
78	Pro	Leu	His	Tyr	Ala	Cys	Phe	Trp	Gly	Gln	Asp	Gln	Val	Ala	Glu	Asp	
79		105					110							115			
81	ctg	gtg	gca	aat	ggg	gcc	ctt	gtc	agc	atc	tgt	aac	aag	tat	gga	gag	558
82	Leu	Val	Ala	Asn	Gly	Ala	Leu	Val	Ser	Ile	Cys	Asn	Lys	Tyr	Gly	Glu	
83		120					125							130			
85	atg	cct	gtg	gac	aaa	gcc	aag	gca	ccc	ctg	aga	gag	ctt	ctc	cga	gag	606
86	Met	Pro	Val	Asp	Lys	Ala	Lys	Ala	Pro	Leu	Arg	Glu	Leu	Leu	Arg	Glu	
87	135					140					145				150		
89	cgg	gca	gag	aag	atg	ggc	cag	aat	ctc	aac	cgt	att	cca	tac	aag	gac	654
90	Arg	Ala	Glu	Lys	Met	Gly	Gln	Asn	Leu	Asn	Arg	Ile	Pro	Tyr	Lys	Asp	
91					155				160						165		
93	aca	tcc	tgg	aag	ggg	acc	acc	cgc	act	cg	ccc	cga	aat	gga	acc	ctg	702
94	Thr	Phe	Trp	Lys	Gly	Thr	Arg	Thr	Arg	Pro	Arg	Asn	Gly	Thr	Leu		
95		170					175							180			
97	aac	aaa	cac	tct	ggc	att	gac	ttc	aaa	cag	ctt	aac	ttc	ctg	acg	aag	750
98	Asn	Lys	His	Ser	Gly	Ile	Asp	Phe	Lys	Gln	Leu	Asn	Phe	Leu	Thr	Lys	
99		185					190							195			
101	ctc	aac	gag	aat	cac	tct	gga	gag	cta	tgg	aag	ggc	cgc	tgg	cag	ggc	798
102	Leu	Asn	Glu	Asn	His	Ser	Gly	Glu	Leu	Trp	Lys	Gly	Arg	Trp	Gln	Gly	
103		200					205							210			
105	aat	gac	att	gtc	gtg	aag	gtg	ctg	aag	cga	gac	tgg	agt	aca	agg		846
106	Asn	Asp	Ile	Val	Val	Lys	Val	Leu	Lys	Val	Arg	Asp	Trp	Ser	Thr	Arg	
107	215					220				225					230		
109	aag	agc	agg	gac	ttc	aat	gaa	gag	tgt	ccc	cg	ctc	agg	att	ttc	tcg	894
110	Lys	Ser	Arg	Asp	Phe	Asn	Glu	Glu	Cys	Pro	Arg	Leu	Arg	Ile	Phe	Ser	
111					235				240						245		
113	cat	cca	aat	gtg	ctc	cca	gtg	cta	gg	gcc	tgc	cag	tct	cca	cct	gct	942
114	His	Pro	Asn	Val	Leu	Pro	Val	Leu	Gly	Ala	Cys	Gln	Ser	Pro	Pro	Ala	
115		250					255							260			
117	cct	cat	cct	act	ctc	atc	aca	cac	tgg	atg	ccg	tat	gga	tcc	ctc	tac	990
118	Pro	His	Pro	Thr	Leu	Ile	Thr	His	Trp	Met	Pro	Tyr	Gly	Ser	Leu	Tyr	
119		265					270							275			
121	aat	gta	cta	cat	gaa	ggc	acc	aat	ttc	gtc	gtg	gac	cag	cag	cgt		1038
122	Asn	Val	Leu	His	Glu	Gly	Thr	Asn	Phe	Val	Val	Asp	Gln	Ser	Gln	Ala	
123		280					285							290			
125	gtg	aag	ttt	gct	ttg	gac	atg	gca	agg	ggc	atg	gcc	ttc	cta	cac	aca	1086
126	Val	Lys	Phe	Ala	Leu	Asp	Met	Ala	Arg	Gly	Met	Ala	Phe	Leu	His	Thr	
127	295					300				305					310		
129	cta	gag	ccc	ctc	atc	cca	cga	cat	gca	ctc	aat	agc	cgt	agt	gta	atg	1134
130	Leu	Glu	Pro	Leu	Ile	Pro	Arg	His	Ala	Leu	Asn	Ser	Arg	Ser	Val	Met	

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131	315	320	325	
133	att gat gag gac atg act gcc cga att agc atg gct gat gtc aag ttc			1182
134	Ile Asp Glu Asp Met Thr Ala Arg Ile Ser Met Ala Asp Val Lys Phe			
135	330	335	340	
137	tct ttc caa tgt cct ggt cgc atg tat gca cct gcc tgg gta gcc ccc			1230
138	Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala Pro Ala Trp Val Ala Pro			
139	345	350	355	
141	gaa gct ctg cag aag cct gaa gac aca aac aga cgc tca gca gac			1278
142	Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr Asn Arg Arg Ser Ala Asp			
143	360	365	370	
145	atg tgg agt ttt gca gtg ctt ctg tgg gaa ctg gtg aca cgg gag gta			1326
146	Met Trp Ser Phe Ala Val Leu Leu Trp Glu Leu Val Thr Arg Glu Val			
147	375	380	385	390
149	ccc ttt gct gac ctc tcc aat atg gag att gga atg aag gtg gca ttg			1374
150	Pro Phe Ala Asp Leu Ser Asn Met Glu Ile Gly Met Lys Val Ala Leu			
151	395	400	405	
153	gaa ggc ctt cgg cct acc atc cca cca ggt att tcc cct cat gtg tgt			1422
154	Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly Ile Ser Pro His Val Cys			
155	410	415	420	
157	aag ctc atg aag atc tgc atg aat gaa gac cct gca aag cga ccc aaa			1470
158	Lys Leu Met Lys Ile Cys Met Asn Glu Asp Pro Ala Lys Arg Pro Lys			
159	425	430	435	
161	ttt gac atg att gtg cct atc ctt gag aag atg cag gac aag			1512
162	Phe Asp Met Ile Val Pro Ile Leu Glu Lys Met Gln Asp Lys			
163	440	445	450	
165	taggactgga aggtccttgc ctgaactcca gaggtgtcgg gacatgttg gggaaatgca			1572
166	cctccccc aa gcagcaggcc tctgggtgcc tcccccgctt ccagtcatgg tactacccca			1632
167	gcctggggtc catccccttc ccccatccct accactgtgc gcaagagggg cgggctcaga			1692
168	gcttgcac ttgccccatg gtgtctccca acatgggagg gatcagcccc gcctgtcaca			1752
169	ataaagttta ttatgaaaaa aaaaaaaaaa aaaaaaaaaa			1789
171	<210> SEQ ID NO: 2			
172	<211> LENGTH: 452			
173	<212> TYPE: PRT			
174	<213> ORGANISM: Homo sapiens			
176	<400> SEQUENCE: 2			
177	Met Asp Asp Ile Phe Thr Gln Cys Arg Glu Gly Asn Ala Val Ala Val			
178	1	5	10	15
179	Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp			
180	20	25	30	
181	His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala			
182	35	40	45	
183	Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn			
184	50	55	60	
185	Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg			
186	65	70	75	80
187	Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val			
188	85	90	95	
189	Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln			
190	100	105	110	

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191 Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile  
 192 115 120 125  
 193 Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu  
 194 130 135 140  
 195 Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn  
 196 145 150 155 160  
 197 Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg  
 198 165 170 175  
 199 Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln  
 200 180 185 190  
 201 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp  
 202 195 200 205  
 203 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val  
 204 210 215 220  
 205 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro  
 206 225 230 235 240  
 207 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala  
 208 245 250 255  
 209 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met  
 210 260 265 270  
 211 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val  
 212 275 280 285  
 213 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly  
 214 290 295 300  
 215 Met Ala Phe Leu His Thr Leu Glu Pro Leu Ile Pro Arg His Ala Leu  
 216 305 310 315 320  
 217 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser  
 218 325 330 335  
 219 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala  
 220 340 345 350  
 221 Pro Ala Trp Val Ala Pro Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr  
 222 355 360 365  
 223 Asn Arg Arg Ser Ala Asp Met Trp Ser Phe Ala Val Leu Leu Trp Glu  
 224 370 375 380  
 225 Leu Val Thr Arg Glu Val Pro Phe Ala Asp Leu Ser Asn Met Glu Ile  
 226 385 390 395 400  
 227 Gly Met Lys Val Ala Leu Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly  
 228 405 410 415  
 229 Ile Ser Pro His Val Cys Lys Leu Met Lys Ile Cys Met Asn Glu Asp  
 230 420 425 430  
 231 Pro Ala Lys Arg Pro Lys Phe Asp Met Ile Val Pro Ile Leu Glu Lys  
 232 435 440 445  
 233 Met Gln Asp Lys  
 234 450  
 237 <210> SEQ ID NO: 3  
 238 <211> LENGTH: 452  
 239 <212> TYPE: PRT  
 240 <213> ORGANISM: Homo sapiens  
 242 <220> FEATURE:

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Input Set : F:\SEQLIST.txt  
Output Set: N:\CRF4\11212002\I840704A.raw

W--> 243 <221> NAME/KEY: Other  
 244 <222> LOCATION: (0)...(0)  
 246 <400> SEQUENCE: 3  
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 248 1 5 10 15  
 249 Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp  
 250 20 25 30  
 251 His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala  
 252 35 40 45  
 253 Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn  
 254 50 55 60  
 255 Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg  
 256 65 70 75 80  
 257 Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val  
 258 85 90 95  
 259 Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln  
 260 100 105 110  
 261 Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile  
 262 115 120 125  
 263 Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu  
 264 130 135 140  
 265 Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn  
 266 145 150 155 160  
 267 Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg  
 268 165 170 175  
 269 Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln  
 270 180 185 190  
 271 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp  
 272 195 200 205  
 273 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val  
 274 210 215 220  
 275 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro  
 276 225 230 235 240  
 277 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala  
 278 245 250 255  
 279 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met  
 280 260 265 270  
 281 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val  
 282 275 280 285  
 283 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly  
 284 290 295 300  
 285 Met Ala Phe Leu His Thr Leu Glu Pro Leu Ile Pro Arg His Ala Leu  
 286 305 310 315 320  
 287 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser  
 288 325 330 335  
 289 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala  
 290 340 345 350  
 291 Pro Ala Trp Val Ala Pro Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr  
 292 355 360 365

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/21/2002  
PATENT APPLICATION: US/09/840,704A TIME: 11:22:40

Input Set : F:\SEQLIST.txt  
Output Set: N:\CRF4\11212002\I840704A.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 2,4,5  
Seq#:17; Xaa Pos. 10,15